

CLAIM AMENDMENT

Please amend the claims as follows

1. (Original) A substantially purified nucleic acid molecule selected from the group consisting of:
 - (a) nucleic acid molecules encoding a phytol kinase polypeptide or polypeptide having phytol kinase activity;
 - (b) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity;
 - (c) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide or a cyanobacterial polypeptide having phytol kinase activity;
 - (d) nucleic acid molecules encoding a phytol kinase polypeptide, or a polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;
 - (e) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 2, 6, and 37-68;
 - (f) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-27, 29-34, and 79;
 - (g) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78;
 - (h) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78, wherein said polypeptide is not derived from *Allium porrum*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*;

- (i) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76;
- (j) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76, wherein said polypeptide is not derived from *Allium porrum*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*;
- (k) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73;
- (l) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73, wherein said polypeptide is not derived from *Synechocystis*, *Aquifex aeolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*, *Rickettsia prowazekii*, *Rickettsia sibirica*, *Synechococcus*, *Thermosynechococcus elongatus*, *Trichodesmium erythraeum* and *Saccharomyces cerevisiae*;
- (m) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70;
- (n) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70, wherein said polypeptide is not derived from *Synechocystis*, *Aquifex aeolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*,

Rickettsia prowazekii, *Rickettsia sibirica*, *Synechoccus*, *Thermosynechoccus elongatus*, *Trichodesmium erythraeum* and *Saccharomyces cerevisiae*;

(o) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-41 and 53-68;

(p) nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity; and

(q) nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 35 and 36.

2. (Original) The substantially purified nucleic acid molecule of claim 1, wherein the plant is selected from the group consisting of *Allium porrum*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza saliva*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*.

3. (Original) The substantially purified nucleic acid molecule of claim 1, wherein the cyanobacteria is selected from the group consisting of *Synechocystis*, *Aquifex aeolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*, *Rickettsia prowazekii*, *Rickettsia sibirica*, *Synechoccus*, *Thermosynechoccus elongatus*, *Trichodesmium erythraeum*; and *Saccharomyces cerevisiae*.

4. (Original) A DNA construct comprising a heterologous promoter that functions in plants operably linked to a nucleic acid molecule selected from the group consisting of:

(a) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 70% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;

(b) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 80% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;

- (c) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 90% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;
- (d) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 95% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 6, 20-68, and 79;
- (e) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 99% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;
- (f) nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;
- (g) nucleic acid molecules comprising a nucleic acid sequence having at least about 80% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;
- (h) nucleic acid molecules comprising a nucleic acid sequence having at least about 90% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;
- (i) nucleic acid molecules comprising a nucleic acid sequence having at least about 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;
- (j) nucleic acid molecules comprising a nucleic acid sequence having at least about 99% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;
- (k) nucleic acid molecules encoding a phytol kinase polypeptide or polypeptides having phytol kinase activity;
- (l) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity;

- (m) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide or a cyanobacterial polypeptide having phytol kinase activity;
- (n) nucleic acid molecules encoding a phytol kinase polypeptide, or a polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;
- (o) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 2, 6, and 37-68;
- (p) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-27, 29-34, and 79;
- (q) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78;
- (r) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78, wherein said polypeptide is not derived from *Allium porrum*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*;
- (s) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76;
- (t) nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76, wherein said polypeptide is not derived from *Allium porruin*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*;

- (u) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73;
- (v) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73, wherein said polypeptide is not derived from *Synechocystis*, *Aquifex aeolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*, *Rickettsia prowazekii*, *Rickettsia sibirica*, *Synechoccus*, *Thermosynechoccus elongatus*, *Trichodesmium erythraeum* and *Saccharomyces cerevisiae*;
- (w) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70;
- (x) nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70, wherein said polypeptide is not derived from *Synechocystis*, *Aquifex aeolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*, *Rickettsia prowazekii*, *Rickettsia sibirica*, *Synechoccus*, *Thermosynechoccus elongatus*, *Trichodesmium erythraeum* and *Saccharomyces cerevisiae*;
- (y) nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity;
- (z) nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 35 and 36; and
- (aa) nucleic acid molecules encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-41 and 53-68.

5. (Currently amended) A transformed plant comprising the nucleic acid molecule~~DNA construct~~ of claim 1.

6. (Original) The transformed plant of claim 5, wherein said plant is selected from the group consisting of alfalfa, *Arabidopsis thaliana*, barley, *Brassica campestris*, oilseed rape, broccoli, cabbage, citrus, canola, cotton, garlic, oat, *Allium*, flax, an ornamental plant, peanut, pepper, potato, rapeseed, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, soybean, chick peas, corn, *Phaseolus*, crambe, mustard, castor bean, sesame, cottonseed, linseed, safflower, and oil palm.

7. (Original) The transformed plant of claim 5, wherein said plant is selected from the group consisting of canola, oilseed rape, and soybean.

8. (Original) The transformed plant of claim 5, wherein said transformed plant comprises tissue with at least one of altered tocopherol and tocotrienol levels relative to a plant with a similar genetic background but lacking said nucleic acid molecule.

9. (Original) The transformed plant of claim 5, wherein said transformed plant produces a seed with at least one of increased tocopherol and tocotrienol levels relative to a plant with a similar genetic background but lacking said nucleic acid molecule.

10. A transformed plant comprising the DNA construct of claim 4:

(1) ~~an introduced nucleic acid molecule selected from the group consisting of:~~

- ~~(a) — nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 70% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;~~
- ~~(b) — nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 80% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;~~
- ~~(c) — nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 90% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;~~
- ~~(d) — nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 95% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;~~
- ~~(e) — nucleic acid molecules encoding a polypeptide comprising an amino acid sequence having at least about 99% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;~~
- ~~(f) — nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(g) — nucleic acid molecules comprising a nucleic acid sequence having at least about 80% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(h) — nucleic acid molecules comprising a nucleic acid sequence having at least about 90% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(i) — nucleic acid molecules comprising a nucleic acid sequence having at least about 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(j) — nucleic acid molecules comprising a nucleic acid sequence having at least about 99 % identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~

- (k) ~~nucleic acid molecules encoding a phytol kinase polypeptide or a polypeptide having phytol kinase activity;~~
- (l) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a polypeptide having phytol kinase activity;~~
- (m) ~~nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide or a polypeptide having phytol kinase activity;~~
- (n) ~~nucleic acid molecules encoding a phytol kinase polypeptide, or a polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;~~
- (o) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 2, 6, and 37-68;~~
- (p) ~~nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-27, 29-34, and 79;~~
- (q) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78;~~
- (r) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78, wherein said polypeptide is not derived from *Allium porrum*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*;~~
- (s) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76;~~
- (t) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group~~

~~consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76, wherein said polypeptide is not derived from *Allium porrum*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*;~~

~~(u) — nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73;~~

~~(v) — nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73, wherein said polypeptide is not derived from *Synechocystis*, *Aquifex aeolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*, *Rickettsia prowazekii*, *Rickettsia sibirica*, *Synechococcus*, *Thermosynechococcus elongatus*, *Trichodesmium erythraeum* and *Saccharomyces cerevisiae*;~~

~~(w) — nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70;~~

~~(x) — nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70, wherein said polypeptide is not derived from *Synechocystis*, *Aquifex aeolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*, *Rickettsia prowazekii*, *Rickettsia sibirica*, *Synechococcus*, *Thermosynechococcus elongatus*, *Trichodesmium erythraeum* and *Saccharomyces cerevisiae*;~~

~~(y) — nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity;~~

~~(z) — nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 35 and 36;~~

~~(aa) — nucleic acid molecules encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-41 and 53-68; and, optionally,~~

~~(2) — an introduced second nucleic acid molecule encoding an enzyme selected from the group consisting of MT1, tMT2, GMT, tyrA, HPT, tocopherol cyclase, chlorophyllase, dxt, dxr, GGPPS, HPPD, AANT1, IDI, and GGH.~~

11. (Original) The transformed plant of claim 10, wherein said plant is selected from the group consisting of alfalfa, *Arabidopsis thaliana*, barley, *Brassica campestris*, oilseed rape, broccoli, cabbage, citrus, canola, cotton, garlic, oat, *Allium*, flax, an ornamental plant, peanut, pepper, potato, rapeseed, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, soybean, chick peas, corn, *Phaseolus*, crambe, mustard, castor bean, sesame, cottonseed, linseed, safflower, and oil palm.

12. (Original) The transformed plant of claim 10, wherein said plant is selected from the group consisting of oilseed rape, soybean and canola.

13. (Original) The transformed plant of claim 10, wherein said transformed plant comprises tissue with at least one of altered tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first nucleic acid molecule.

14. (Original) The transformed plant of claim 10, wherein said transformed plant produces a seed with at least one of increased tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first nucleic acid molecule.

15. (Original) The transformed plant of claim 10, wherein said transformed plant comprises tissue with at least one of altered tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first and second nucleic acid molecules.

16. (Original) The transformed plant of claim 10, wherein said transformed plant produces a seed with at least one of increased tocopherol or tocotrienol levels relative to a plant with similar genetic background but lacking said introduced first and second nucleic acid molecules.

17. (Currently amended) The transformed plant of claim 3740, wherein the second introduced nucleic acid molecule comprises one or more of SEQ ID NOs: 13-16, and 18 or 19.

18. (Currently amended) A method for increasing at least one of tocopherol and tocotrienol levels in a plant comprising transforming ~~at~~ the plant with the DNA construct of claim 4

~~(1) — an introduced nucleic acid molecule selected from the group consisting of:~~

~~(a) — nucleic acid molecules encoding an amino acid sequence having at least about 70% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 6, 20-68, and 79;~~

~~(b) — nucleic acid molecules encoding an amino acid sequence having at least about 80% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 6, 20-68, and 79;~~

~~(c) — nucleic acid molecules encoding an amino acid sequence having at least about 90% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 6, 20-68, and 79;~~

~~(d) — nucleic acid molecules encoding an amino acid sequence having at least about 95% identity to an amino acid sequence selected from the group consisting of SEQ ID NO: 2, 6, 20-68, and 79;~~

- ~~(e) — nucleic acid molecules encoding an amino acid sequence having at least about 99% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;~~
- ~~(f) — nucleic acid molecules comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(g) — nucleic acid molecules comprising a nucleic acid sequence having at least about 80% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(h) — nucleic acid molecules comprising a nucleic acid sequence having at least about 90% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(i) — nucleic acid molecules comprising a nucleic acid sequence having at least about 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(j) — nucleic acid molecules which comprise a nucleic acid sequence having at least about 99% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 5, and 17;~~
- ~~(k) — nucleic acid molecules encoding a phytol kinase polypeptide or polypeptide having phytol kinase activity;~~
- ~~(l) — nucleic acid molecules encoding a plant phytol kinase polypeptide, or a polypeptide having phytol kinase activity;~~
- ~~(m) — nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide or cyanobacterial polypeptide having phytol kinase activity;~~
- ~~(n) — nucleic acid molecules encoding a phytol kinase polypeptide, or a polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 20-68, and 79;~~

- (c) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 2, 6, and 37-68;~~
- (p) ~~nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-27, 29-34, and 79;~~
- (q) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78;~~
- (r) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid selected from the group consisting of SEQ ID NOs: 74, 77, and 78, wherein said polypeptide is not derived from *Allium porrum*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*;~~
- (s) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76;~~
- (t) ~~nucleic acid molecules encoding a plant phytol kinase polypeptide, or a plant polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 74, 77, and 78 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 75 and 76, wherein said polypeptide is not derived from *Allium porrum*, *Brassica napus*, *Gossypium*, *Glycine max*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*;~~
- (u) ~~nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 71, 72, and 73;~~
- (v) ~~nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising an amino acid sequence~~

~~selected from the group consisting of SEQ ID NOs: 71, 72, and 73, wherein said polypeptide is not derived from *Synechocystis*, *Aquifex acolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*, *Rickettsia prowazekii*, *Rickettsia sibirica*, *Synechococcus*, *Thermosynechococcus elongatus*, *Trichodesmium erythraeum* and *Saccharomyces cerevisiae*;~~

~~(w) — nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70;~~

~~(x) — nucleic acid molecules encoding a cyanobacterial phytol kinase polypeptide, or a cyanobacterial polypeptide having phytol kinase activity, comprising one or more amino acid sequences selected from the group consisting of SEQ ID NOs: 71, 72, and 73 and further comprising an amino acid sequence comprising one or more of SEQ ID NOs: 69 and 70, wherein said polypeptide is not derived from *Synechocystis*, *Aquifex acolicus*, *Chlorobium tepidum*, *Chloroflexus aurantiacus*, *Nostoc punctiforme*, *Prochlorococcus marinus*, *Rickettsia conorii*, *Rickettsia prowazekii*, *Rickettsia sibirica*, *Synechococcus*, *Thermosynechococcus elongatus*, *Trichodesmium erythraeum* and *Saccharomyces cerevisiae*;~~

~~(y) — nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity;~~

~~(z) — nucleic acid molecules encoding a yeast phytol kinase polypeptide, or a yeast polypeptide having phytol kinase activity, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 35 and 36;~~

~~(aa) — nucleic acid molecules encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-41 and 53-68; and optionally,~~

~~(2) — an introduced second nucleic acid molecule encoding an enzyme selected from the group consisting of MT1, tMT2, GMT, tyrA, HPT, tocopherol cyclase, chlorophyllase, dxs, dxr, GGPPS, HPPD, AANT1, IDI, and GGH; and~~

(3)——growing said plant, wherein said plant has at least one of an increased tocopherol and tocotrienol level as compared to a plant with a similar genetic background but lacking said introduced nucleic acid molecule(s).

19. (Original) The method of claim 18, wherein said plant is selected from the group consisting of alfalfa, *Arabidopsis thaliana*, barley, *Brassica campestris*, oilseed rape, broccoli, cabbage, citrus, canola, cotton, garlic, oat, *Allium*, flax, an ornamental plant, peanut, pepper, potato, rapeseed, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, soybean, chick peas, corn, *Phaseolus*, crambe, mustard, castor bean, sesame, cottonseed, linseed, safflower, and oil palm.

20. (Original) The method of claim 18, wherein said plant is selected from the group consisting of oilseed rape, soybean and canola.

21. (Original) The method of claim 18, wherein said transformed plant comprises tissue with at least one of altered tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first nucleic acid molecule.

22. (Original) The method of claim 18, wherein said transformed plant produces a seed with at least one of increased tocopherol or tocotrienol levels relative to a plant with a similar genetic background but lacking said introduced first nucleic acid molecule.

23. (Currently amended) The method of claim ~~3~~18, wherein the second introduced nucleic acid molecule comprises one or more of SEQ ID NOs: 13-16, and 18 or 19.

24. (Currently amended) Seed from the plant of claim 10 comprising the DNA construct.

25-29. (Canceled)

30. (Original) A method for increasing the ability of a plant to withstand a stress, the method comprising incorporating into one or more cells of the plant a DNA construct comprising

- (a) an heterologous promoter;
- (b) a DNA encoding a phytol kinase; and
- (c) a 3' untranslated region containing a functional polyadenylation signal wherein expression of the DNA construct increases the ability of the plant to withstand the stress.

31. (Original) A plant cell transformed with a DNA construct encoding a phytol kinase that confers stress to a plant regenerated from said plant cell.

32. (Original) A transgenic plant regenerated from the plant cell of claim 31.

33. (Original) A seed produced by the transgenic plant of claim 32.

34. (Original) The method of claim 26, wherein a DNA molecule encoding a plastid transit peptide is positionally located and operably linked between the promoter and the DNA molecule encoding the phytol kinase.

35. (Original) A method of increasing the production of tocotrienols in a plant comprising:
(a) transforming a plant cell with a nucleic acid construct which causes the down regulation of SEQ ID NOs: 1, 5, or 17 or a nucleic acid sequence having at least about 80% identity to such sequence; (b) growing the transformed plant cell into a fertile plant; and (c) selecting for a plant with increased tocotrienol levels.

36. (Original) The method of claim 35 wherein down regulation is accomplished through dsRNAi, antisense suppression or sense suppression.

Please add new claims 37-38 as follows:

37. (New) The transformed plant of claim 10, further comprising an introduced second nucleic acid molecule encoding an enzyme selected from the group consisting of MT1, tMT2, GMT, tyrA, HPT, tocopherol cyclase, chlorophyllase, dxs, dxr, GGPPS, HPPD, AANT1, IDI, and GGH.

38. (New) The method of claim 18, further comprising transforming the plant with an introduced second nucleic acid molecule encoding an enzyme selected from the group consisting of MT1, tMT2, GMT, tyrA, HPT, tocopherol cyclase, chlorophyllase, dxs, dxr, GGPPS, HPPD, AANT1, IDI, and GGH.